Attorney Docket No: NU-593XX
Inventor(s): Mary Jo Ondrechen et al.
Application No.: 10/678,756
TC Art Unit: 1631/Examiner: Larry D. Riggs II
OA Date: 09/17/2007/Resp. Date: 01/17/07

REMARKS

New claim 17, dependent on claim 2, has been added herein. Applicants submit that the new claim is fully supported in the specification, e.g., in the paragraphs at p. 6, lines 12-31, and that no new matter has been added.

Thus, claims 1-17 are now pending in the instant application. The Applicants appreciate the Examiner's summary that:

1) The *In re Katz* Declaration of lead inventor Mary Jo Ondrechen has been considered;

2) The question of the priority claim has been withdrawn;

3) The objection to browser-executable code in the specification has been withdrawn;

4) The rejection under 35 USC § 101 has been withdrawn; and

5) The rejection of claims 1-3 and 6-16 under 35 USC § 112 as failing to comply with the written description requirement has been withdrawn.

Rejection under 35 USC § 112 for Lack of Enablement

Claims 1-16 are newly rejected as failing to comply with the enablement requirement, the Examiner stating that the specification, while being enabling for determining interaction sites in a protein of experimentally determined structures, does not reasonably provide enablement for determining interaction sites in protein structures not experimentally determined. This new rejection is respectfully traversed in light of the following remarks, and reconsideration is requested.

As stated in the application at p. 5, lines 13-15, the method of the invention is directed to predicting protein function from sequence and structure information, even in the absense of biochemical data. This statement was not meant to imply that the inventors felt their contribution was in determining the protein three-dimensional structure itself. To remove any possible ambiguity in this regard, the Applicants have amended the preamble of claim 1 to recite that the method is directed to a "method for determining interaction sites in a protein having an identified three-dimensional structure." Applicants have also added as a first step of the method "providing an identified three-dimensional structure for said protein" on which the heart of the method is then practiced. This structure can be obtained, e.g., experimentally by the practitioners of the Applicants' method or downloaded from a database or or determined as a theoretical model structure.

The Examiner has accepted that the Applicants' specification is "enabling for determining interaction sites in a protein of experimentally determined structures" (Office Action, p. 3). Presumably, the Examiner also accepts that proteins having experimentally determined structures include those downloaded from a database as well as those determined by the practioners of the Applicants' method.

However, the Examiner then states at p. 4 of the Office Action that practicing of the Applicants' method starting by theoretically predicting the structure to be analyzed using a modeling method is not enabled. The Examiner is referred to the accompanying Declaration of co-inventor Mary Jo Ondrechen.

In the Declaration, Dr. Ondrechen states that protein three-dimensional structure can be theoretically predicted using a modeling method. Comparative/homology modeling is an accepted method of protein structure determination, in use well before the instant application was filed. As an example, Dr. Ondrechen pointed to SWISS-MODEL (http://swissmodel.expasy.org), an automated comparative protein modeling server, which was initiated in 1993. Its purpose is "to make protein modeling accessible to all biochemists and molecular biologists world wide." A printout of several pages from this website, including the abstract of a paper by the initiator of the modeling server, are attached to the Ondrechen Declaration.

The Declaration also states that, in work completed since this application was filed, the Applicants carried out a large scale experiment using the method of the invention to locate the active site in 21 sets of protein structures built by comparative modeling. An abstract of Shehadi et al., Active site prediction for comparative model structures with THEMATICS. Journal of Bioinformatics and Computational Biology (2005), 3(1), 127-143, showing these results is also attached to the Declaration and a full copy of this journal article will follow shortly. Dr. Ondrechen pointed out that the method of the invention was shown to correctly locate the active site in the model structures.

Thue, Applicants submit that all of the pending claims are fully supported in the specification and the rejection has been overcome.

Rejection under 35 USC § 112 for Failing to Comply with the Written Description Requirement

The Examiner has also continued the previous rejection of claim 5 for failing to comply with the written description requirement. The Examiner contends that the Applicants were not in possession of a "representative number" of examples of determining the structure of the protein to be analyzed for putative interaction sites.

The Examiner cites to Xu et al. (2000) as disclosing that protein structure prediction mechanisms are "extremely difficult" and "generally unreliable." However, other practictioners of protein modeling have stated differently. The Patent Office itself cited one such reference (Sali, 1998, Nature Structural Biology, 5, 1029-1032) in the previous Office Action dated March 22, 2007 (p. 12, last paragraph - p. 13, end of first paragraph) in an obviousness rejection of claim 5, stating:

> It would have been obvious to a person of ordinary skill in the art at the time the invention was made to modify the predictive method of Ondrechen et al. such that they allowed for the determination of a protein's structure from its amino acid sequence. One having ordinary skill in the art would have been motivated to do this because, as suggested by Sali, "it is not feasible to determine the structure of every protein by experiment," and obtaining structures from amino acid sequence would would allow one to analyze, "three-dimensional models for hundreds of thousands of . . . proteins," from 10,000 protein structures, (page 1029, 1st column, 1st paragraph, lines 15-18).

Thus, Applicants submit that this rejection has been made moot by a previous citation from the Patent Office in this same prosecution. Furthermore, as described above, the Ondrechen Declaration points out another set of prior art references that counter the Examiner's assertion. Thus, Applicants submit that this rejection has been overcome.

The Applicants submit that all claims in the application are in condition for allowance and such action is requested.

The Examiner is encouraged to telephone the undersigned attorney to discuss any matter that would expedite allowance of the present application.

Respectfully submitted,

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